Amendments to the Specification:

With reference to the Substitute Specification, please amend the heading at page 3, line 16 as follows:

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Brief Description of the Several Views of the Drawing.

With reference to the Substitute Specification, please amend the paragraph at page 3, lines 19-21 as follows:

Figs. ~~2a~~ 2A and ~~2b~~ 2B schematically demonstrate side and front views of a comparison of the crystal structures of free hGHR and hGHR interacting with hGH site 1 in the 1:2 complex; and

With reference to the Substitute Specification, please amend the paragraph at page 6, lines 13-21 as follows:

Figs ~~2a~~ 2A and ~~2b~~ 2B schematically demonstrate a comparison of the crystal structures of free hGHR and hGHR interacting with hGH site 1 in the 1:2 complex. In the structural alignment, only the C-terminal domains were used (residues 128-234) in order to clearly visualize the domain-domain movements upon transitions from free to complexed form, wherein Fig. ~~2a~~ 2A is a side view and Fig. ~~2b~~ 2B is a front view. In the free receptor crystal, the two hGHR molecules in the asymmetric unit are very similar with a root mean square deviation of 0.18 Å comparing 184 Ca positions. The corresponding values for the liganded receptors in the 1:2 complex are 1.04 Å (181 Ca positions) and 1.17 Å (172 Ca positions) for the hGH site 1 and site 2 binding receptor respectively.